



SEQUENCE LISTING

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HIKICHI, Yuichi
NISHIMURA, Atsushi

<120> Novel Protein and DNA Thereof

<130> PF613TD1

<140> US 10/726,148

<141> 2003-12-02

<150> US 09/786,256

<151> 2001-03-02

<150> PCT/JP99/04766

<151> 1999-09-02

<150> JP 10-250115

<151> 1998-09-03

<160> 32

<170> PatentIn version 3.0

<210> 1

<211> 540

<212> PRT

<213> Homo sapiens

<220>

<221> PEPTIDE

<222> (1)..(540)

<223> An isolated ADAM family protein

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1 5 10 15

Ser Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr
20 25 30

Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu
35 40 45

Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn
50 55 60

Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala
65 70 75 80

Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr
85 90 95

Thr Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu
 100 105 110
 Asn Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg
 115 120 125
 Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser
 130 135 140
 Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro
 145 150 155 160
 Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp
 165 170 175
 Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val
 180 185 190
 Lys Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr
 195 200 205
 Tyr Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln
 210 215 220
 Asp Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met
 225 230 235 240
 Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile
 245 250 255
 Trp Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr
 260 265 270
 Leu Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys
 275 280 285
 Arg His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr
 290 295 300
 Thr Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val
 305 310 315 320
 Gly Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr
 325 330 335
 Met Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr
 340 345 350
 Ser Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser
 355 360 365
 Phe Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp
 370 375 380
 Lys Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu
 385 390 395 400
 Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu
 405 410 415

Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile
420 425 430

Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala
435 440 445

Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val
450 455 460

Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly
465 470 475 480

Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro
485 490 495

Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu
500 505 510

Gln Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Arg Arg Thr Asn Pro
515 520 525

Phe Pro Cys Ala Cys Ala Lys Glu Asn His Phe Arg
530 535 540

<210> 2
<211> 96
<212> PRT
<213> Homo sapiens

<220>
<221> PEPTIDE
<222> (1)..(96)
<223> Isolated fragment of Protein of Seq ID No.1 (aa 400-495)

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Leu Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val
1 5 10 15

Glu Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn
20 25 30

Ile Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys
35 40 45

Ala Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met
50 55 60

Val Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn
65 70 75 80

Gly Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe
85 90 95

<210> 3
<211> 1620
<212> DNA
<213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(1620)
 <223> Isolated DNA encoding for the protein of SEQ ID NO.1

<400> 3
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 gaactccctg ggggtgaagaa gtatgaagtg gttttatccta taagacttca tccactgcat 120
 aaaagagagg ccaaagagcc agagcaacag gaacaatttg aaactgaatt aaagtataaa 180
 atgacaatta atggaaaaat tgcagtgcctt tatttgaaaa aaaacaagaa cctccttgca 240
 ccaggctaca cggaacata ttataattcc actggaaagg agatcaccac aagcccacaa 300
 attatggatg attgttatta tcaaggacat attcttaagt aaaaggtttc tgacgctagc 360
 atcagcacat gtaggggtctt aaggggctac ttcagtcagg gggatcaaag atactttatt 420
 gaacctttta gccccatata tcgggatgga caggagcatg cactcttcaa gtataaccct 480
 gatgaaaaga attatgacag cacctgtggg atggatgggtg tgttggtgggc ccacgatttg 540
 cagcagaaca ttgccctacc tgccaccaa ctagtaaaat tgaaagacag gaaggttcag 600
 gaacatgaga aatacataga atattatttg gtcctggata atggtgagtt taaaagggtac 660
 aatgagaatc aagatgagat cagaaagagg gtatttgaga tggctaatta tgtcaacatg 720
 ctttataaaa agctcaatac tcatgtggcc ttagtgggtg tggaaatctg gactgacaag 780
 gataagataa agataacccc aaatgcaagc ttcaccttgg agaatttttc taaatggagg 840
 gggagtgttc tctcaagaag aaagcgtcat gatattgtct agttaatcac agcaacagaa 900
 cttgtctgga cgactgtggg tcttgcatth atgtctacaa tgtgttctcc ttattctgtt 960
 ggcgttgttc aggaccacag cgataatctt cttagagttg cagggacaat ggcacatgaa 1020
 atgggccaca actttggaat gtttcatgac gactattctt gcaagtgtcc ttctacaata 1080
 tgtgtgatgg acaaagcact gagcttctat ataccacag acttcagttc ctgcagccgt 1140
 ctgagctatg acaagttttt tgaagataaa ttatcaaatt gcctctttta tgctccattg 1200
 cctacagata tcatatccac tccaatttgt ggggaaccagt tgggtggaaat gggagaggac 1260
 tgtgatgttg ggacatctga ggaatgtacc aatatttgtc gtgatgctaa gacatgtaaa 1320
 atcaaagcaa cttttcaatg tgcattagga gaatgttgtg aaaaatgcca atttaaaaag 1380
 gctgggatgg tgtgcagacc agcaaaagat gagtgcgacc tgctgaaat gtgtaatggt 1440
 aaatctggta attgtcctga tgatagattc caagtcaatg gcttcccttg ccatcacggg 1500
 aagggccact gcttgatggg gacatgcccc acactgcagg agcagtgcac agagctgtgg 1560
 ggaccaggta ggaggacaaa tcctttcccc tgtgcatgtg cgaaggaaaa tcatttcaga 1620

<210> 4
 <211> 288
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(288)
 <223> Artificial DNA encoding for peptide of SEQ ID NO.2

<400> 4
 ttgcctacag atatcatatc cactccaatt tgtgggaacc agttgggtgga aatgggagag 60
 gactgtgatt gtgggacatc tgaggaatgt accaatatth gctgtgatgc taagacatgt 120
 aaaatcaaag caacttttca atgtgcatta ggagaatgtt gtgaaaaatg ccaattttaa 180
 aaggctggga tgggtgtcag accagcaaaa gatgagtgcg acctgcctga aatgtgtaat 240
 ggtaaactctg gtaattgtcc tgatgataga ttccaagtca atggcttc 288

<210> 5
 <211> 201
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(201)
 <223> Isolated fragment of protein of SEQ ID NO.1 (aa 199-399)

 <400> 5
 Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr Leu Val Leu Asp Asn
 1 5 10 15
 Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp Glu Ile Arg Lys Arg
 20 25 30
 Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu Tyr Lys Lys Leu Asn
 35 40 45
 Thr His Val Ala Leu Val Gly Met Glu Ile Trp Thr Asp Lys Asp Lys
 50 55 60
 Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr Leu Glu Asn Phe Ser Lys
 65 70 75 80
 Trp Arg Gly Ser Val Leu Ser Arg Arg Lys Arg His Asp Ile Ala Gln
 85 90 95
 Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr Thr Val Gly Leu Ala Phe
 100 105 110
 Met Ser Thr Met Cys Ser Pro Tyr Ser Val Gly Val Val Gln Asp His
 115 120 125
 Ser Asp Asn Leu Leu Arg Val Ala Gly Thr Met Ala His Glu Met Gly
 130 135 140
 His Asn Phe Gly Met Phe His Asp Asp Tyr Ser Cys Lys Cys Pro Ser
 145 150 155 160
 Thr Ile Cys Val Met Asp Lys Ala Leu Ser Phe Tyr Ile Pro Thr Asp
 165 170 175
 Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp Lys Phe Phe Glu Asp Lys
 180 185 190
 Leu Ser Asn Cys Leu Phe Asn Ala Pro
 195 200

 <210> 6
 <211> 10
 <212> PRT
 <213> Homo sapiens

 <220>
 <221> PEPTIDE
 <222> (1)..(10)
 <223> Isolated fragment of Protein of SEQ ID NO.1 (aa 428-437)

 <400> 6
 Glu Cys Thr Asn Ile Cys Cys Asp Ala Lys

1	5	10
<210> 7		
<211> 23		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Nucleic Acid primer		
<220>		
<221> misc_feature		
<222> (6)..(6)		
<223> n equals a, t, g, or c		
<400> 7		
gtrgansmdk sdgarsartg tga		23
<210> 8		
<211> 26		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Nucleic Acid primer		
<220>		
<221> misc_feature		
<222> (13)..(13)		
<223> n equals a, t, g, or c		
<220>		
<221> misc_feature		
<222> (21)..(21)		
<223> n equals a, t, g, or c		
<400> 8		
ayytgwdbrd dwncdkvdds ngggca		26
<210> 9		
<211> 28		
<212> DNA		
<213> Artificial sequence		
<220>		
<223> Nucleic Acid primer		
<400> 9		
atcacagtcc tctccattt ccaccaac		28
<210> 10		
<211> 26		
<212> DNA		
<213> Artificial sequence		

<220>
 <223> Nucleic Acid Primer

 <400> 10
 cacatttcag gcaggtcgca ctcac 26

 <210> 11
 <211> 27
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Nucleic Acid Primer

 <400> 11
 tcgctgtggt cctgaacaac gccaaca 27

 <210> 12
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Nucleic Acid Primer

 <400> 12
 cacaccatcc atcccacagg tgctgtca 28

 <210> 13
 <211> 28
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Nucleic Acid Primer

 <400> 13
 ggaaccagtt ggtggaaatg ggagagga 28

 <210> 14
 <211> 29
 <212> DNA
 <213> Artificial sequence

 <220>
 <223> Nucleic Acid Primer

 <400> 14
 aggactgtga ttgtgggacg tctgaggaa 29

<210> 15
 <211> 775
 <212> PRT
 <213> Homo sapiens

<220>
 <221> PEPTIDE
 <222> (1)..(775)
 <223> An isolated ADAM family protein

<400> 15
 Met Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Leu Ser Val Ala Val
 1 5 10 15
 Ser Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr
 20 25 30
 Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu
 35 40 45
 Gln Gln Glu Gln Trp Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn
 50 55 60
 Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala
 65 70 75 80
 Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr
 85 90 95
 Thr Ser Pro Gln Ile Met Trp Trp Trp Tyr Tyr Gln Gly His Ile Leu
 100 105 110
 Asn Glu Lys Val Ser Trp Ala Ser Ile Ser Thr Trp Arg Gly Leu Arg
 115 120 125
 Gly Tyr Trp Ser Gln Gly Trp Gln Arg Tyr Trp Ile Glu Pro Leu Ser
 130 135 140
 Pro Ile His Arg Trp Gly Gln Glu His Ala Leu Trp Lys Tyr Asn Pro
 145 150 155 160
 Trp Glu Lys Asn Tyr Trp Ser Thr Trp Gly Met Trp Gly Val Leu Trp
 165 170 175
 Ala His Trp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val
 180 185 190
 Lys Leu Lys Trp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr
 195 200 205
 Tyr Leu Val Leu Trp Asn Gly Glu Trp Lys Arg Tyr Asn Glu Asn Gln
 210 215 220
 Trp Glu Ile Arg Lys Arg Val Trp Glu Met Ala Asn Tyr Val Asn Met
 225 230 235 240
 Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile
 245 250 255

Gly Arg Ile Val Thr Trp Leu Thr Trp Lys Thr Trp Trp Pro Glu Trp
 580 585 590
 Thr Ser Gln Glu Ile Gly Met Val Ala Asn Gly Thr Lys Trp Gly Trp
 595 600 605
 Asn Lys Val Trp Ile Asn Ala Glu Trp Val Trp Ile Glu Lys Ala Tyr
 610 615 620
 Lys Ser Thr Asn Trp Ser Ser Lys Trp Lys Gly His Ala Val Trp Trp
 625 630 635 640
 His Glu Leu Gln Trp Gln Trp Glu Glu Gly Trp Ile Pro Pro Trp Trp
 645 650 655
 Trp Trp Ser Ser Val Val Trp His Trp Ser Ile Val Val Gly Val Leu
 660 665 670
 Trp Pro Met Ala Val Ile Trp Val Val Val Ala Met Val Ile Arg His
 675 680 685
 Gln Ser Ser Arg Glu Lys Gln Lys Lys Trp Gln Arg Pro Leu Ser Thr
 690 695 700
 Thr Gly Thr Arg Pro His Lys Gln Lys Arg Lys Pro Gln Met Val Lys
 705 710 715 720
 Ala Val Gln Pro Gln Glu Met Ser Gln Met Lys Pro His Val Tyr Trp
 725 730 735
 Leu Pro Val Glu Gly Asn Glu Pro Pro Ala Ser Trp His Lys Trp Thr
 740 745 750
 Asn Ala Leu Pro Pro Thr Val Trp Lys Trp Asn Pro Met Ser Thr Pro
 755 760 765
 Lys Trp Ser Asn Pro Lys Ala
 770 775

<210> 16
 <211> 2325
 <212> DNA
 <213> Homo sapiens

<220>
 <221> misc_feature
 <222> (1)..(2325)
 <223> Isolated nucleic acid encoding for a protein of SEQ ID NO. 15

<400> 16
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 gaactccctg ggggtgaagaa gtatgaagtg gtttataccta taagacttca tccactgcat 120
 aaaagagagg ccaaagagcc agagcaacag gaacaatttg aaactgaatt aaagtataaa 180
 atgacaatta atggaaaaat tgcagtgctt tatttgaaaa aaaacaagaa cctccttgca 240
 ccagggtaca cggaaacata ttataattcc actggaaagg agatcaccac aagcccacaa 300
 attatggatg attgttatta tcaaggacat attcttaatg aaaagggttc tgacgctagc 360
 atcagcacat gtaggggtct aaggggctac ttcagtcagg gggatcaaag atactttatt 420
 gaacctttaa gccccatata tcgggatgga caggagcatg cactcttcaa gtataaccct 480

gatgaaaaga	attatgacag	cacctgtggg	atggatgggtg	tgttgtgggc	ccacgatttg	540
cagcagaaca	ttgccctacc	tgccaccaa	ctagtaaaat	tgaagacag	gaaggttcag	600
gaacatgaga	aatacataga	atattatttg	gtcctggata	atggtgagtt	taaaaggtag	660
aatgagaatc	aagatgagat	cagaaagagg	gtatttgaga	tggctaatta	tgtcaacatg	720
ctttataaaa	agctcaatac	tcatgtggcc	ttagttggta	tggaaatctg	gactgacaag	780
gataagataa	agataacccc	aaatgcaagc	ttcaccttgg	agaatttttc	taaatggagg	840
gggagtgttc	tctcaagaag	aaagcgtcat	gatattgctc	agttaatcac	agcaacagaa	900
cttgctggaa	cgactgtggg	tcttgcatth	atgtctacaa	tgtgttctcc	ttattctgth	960
ggcgttgthc	aggaccacag	cgataatctt	cttagagthg	cagggacaat	ggcacatgaa	1020
atggggccaca	actttggaat	gtttcatgac	gactattctt	gcaagtgtcc	ttctacaata	1080
tgtgtgatgg	acaaagcact	gagcttctat	ataccacacag	acttcagthc	ctgcagccgt	1140
ctcagctatg	acaagththt	tgaagataaa	ttatcaaatt	gcctctthta	tgctccattg	1200
cctacagata	tcatatccac	tccaattthg	gggaaccagt	tggtggaatt	gggagaggag	1260
tgtgattgtg	ggacatctga	ggaatgtacc	aatatttgct	gtgatgctaa	gacatgtaaa	1320
atcaaagcaa	ctthttcaatg	tgcattagga	gaatgttgtg	aaaaatgcca	atttaaaaag	1380
gctgggatgg	tgtgcagacc	agcaaaagat	gagtgcgacc	tgcttgaaat	gtgtaatggt	1440
aaatctggta	attgtcctga	tgatagattc	caagtcaatg	gcttcccttg	ccatcacggg	1500
aagggccact	gcttgatggg	gacatgcccc	acactgcagg	agcagtgcac	agaactgtgg	1560
ggaccaggaa	ctgaggtthc	agataagtca	tgttacaaca	ggaatgaagg	tgggtcaaag	1620
tacgggtact	gtcgcagagt	ggatgacaca	ctcattccct	gcaaagcaaa	tgataccatg	1680
tgtgggaagt	tgthctgtca	aggtgggtcg	gataattthc	cctggaaagg	acggatagtg	1740
actthctctga	catgtaaaac	atttgatcct	gaagacacaa	gtcaagaaat	aggcatggtg	1800
gccaatggaa	ctaagtgtgg	cgataacaag	gtthtgatta	atgcagaatg	tgtggatatt	1860
gagaaagcct	acaaatcaac	caattgctca	tctaagtgca	aaggacatgc	tgtgtgtgac	1920
catgagctcc	agtgtcaatg	tgaggaagga	tggatccctc	ccgactgcga	tgactcctca	1980
gtggctcttc	actthctccat	tgtggttggg	gtgctgtthc	caatggcggt	cattthttgtg	2040
gtggttgcta	tggtaatccg	gcaccagagc	tccagagaaa	agcagaagaa	agatcagagg	2100
ccactatcta	ccactggcac	caggccacac	aaacagaaga	ggaaacccca	gatggtaaag	2160
gctgttcaac	cccaagagat	gagtcagatg	aagccccatg	tgtatgatct	gccagtagaa	2220
ggcaatgagc	ccccagcctc	thttcataaa	gacacaaacg	cactthcccc	tactgtthtc	2280
aaggataatc	caatgtctac	acctaaggac	tcaaattcaa	aagca		2325

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 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 17
 catatggthc aggaacatga gaaatacata 30

<210> 18
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 18
 ctcgaggaag ccattgactt ggaatctatc 30

<210> 19

<211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 19
 ctcagatgtc ccacaatcac agtc 24

<210> 20
 <211> 25
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 20
 acatgtaaaa tcaaagcaac ttttc 25

<210> 21
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 21
 gtggtggtgg acaactagga aactctgg 28

<210> 22
 <211> 24
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 22
 cgaggcgaat catggctcac cgcg 24

<210> 23
 <211> 30
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 23
 tccacgcgtt tgggaaactt cttggctgcg 30

<210> 24
 <211> 29
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 24
 gcttcgtcgc cgctacgcgt ggggccgga 29

<210> 25
 <211> 27
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 25
 atcgattgag cgagaagagc agacacc 27

<210> 26
 <211> 28
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 26
 agatcttgcc atccagattt tccagttt 28

<210> 27
 <211> 20
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleic Acid Primer

<400> 27
 cgccgctggg ctgccgggtc 20

<210> 28
 <211> 20
 <212> DNA

<213> Artificial sequence

<220>

<223> Nucleic Acid Primer

<400> 28

tccatcccga tgtatggggc

20

<210> 29

<211> 2560

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (55)..(1674)

<220>

<221> misc_feature

<222> (1)..(2560)

<223> DNA sequence of FIG 1-2 containing SEQ ID NO:3 encoding for protein of SEQ ID NO:1

<220>

<221> mat_peptide

<222> (55)..()

<400> 29

gcagcaccca cctgagcgag aagagcagac accgtgctcc tggaatcacc cagc atg 57
Met
1

ttg caa ggt ctc ctg cca gtc agt ctc ctc ctc tct gtt gca gta agt 105
Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Ser Val Ala Val Ser
5 10 15

gct ata aaa gaa ctc cct ggg gtg aag aag tat gaa gtg gtt tat cct 153
Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr Pro
20 25 30

ata aga ctt cat cca ctg cat aaa aga gag gcc aaa gag cca gag caa 201
Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu Gln
35 40 45

cag gaa caa ttt gaa act gaa tta aag tat aaa atg aca att aat gga 249
Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn Gly
50 55 60 65

aaa att gca gtg ctt tat ttg aaa aaa aac aag aac ctc ctt gca cca 297
Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala Pro
70 75 80

ggc tac acg gaa aca tat tat aat tcc act gga aag gag atc acc aca 345
Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr Thr
85 90 95

agc cca caa att atg gat gat tgt tat tat caa gga cat att ctt aat	393
Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu Asn	
100 105 110	
gaa aag gtt tct gac gct agc atc agc aca tgt agg ggt cta agg ggc	441
Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg Gly	
115 120 125	
tac ttc agt cag ggg gat caa aga tac ttt att gaa cct tta agc ccc	489
Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser Pro	
130 135 140 145	
ata cat cgg gat gga cag gag cat gca ctc ttc aag tat aac cct gat	537
Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro Asp	
150 155 160	
gaa aag aat tat gac agc acc tgt ggg atg gat ggt gtg ttg tgg gcc	585
Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp Ala	
165 170 175	
cac gat ttg cag cag aac att gcc cta cct gcc acc aaa cta gta aaa	633
His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val Lys	
180 185 190	
ttg aaa gac agg aag gtt cag gaa cat gag aaa tac ata gaa tat tat	681
Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr	
195 200 205	
ttg gtc ctg gat aat ggt gag ttt aaa agg tac aat gag aat caa gat	729
Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp	
210 215 220 225	
gag atc aga aag agg gta ttt gag atg gct aat tat gtc aac atg ctt	777
Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu	
230 235 240	
tat aaa aag ctc aat act cat gtg gcc tta gtt ggt atg gaa atc tgg	825
Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile Trp	
245 250 255	
act gac aag gat aag ata aag ata acc cca aat gca agc ttc acc ttg	873
Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr Leu	
260 265 270	
gag aat ttt tct aaa tgg agg ggg agt gtt ctc tca aga aga aag cgt	921
Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys Arg	
275 280 285	
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His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr Thr	
290 295 300 305	
gtg ggt ctt gca ttt atg tct aca atg tgt tct cct tat tct gtt ggc	1017
Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val Gly	
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Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr Met	
325 330 335	

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Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr Ser	
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Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser Phe	
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Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp Lys	
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Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu Pro	
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Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu Met	
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Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile Cys	
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Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala Leu	
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Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val Cys	
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Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly Lys	
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tct ggt aat tgt cct gat gat aga ttc caa gtc aat ggc ttc cct tgc	1545
Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro Cys	
485 490 495	
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His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu Gln	
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Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Arg Arg Thr Asn Pro Phe	
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ccc tgt gca tgt gcg aag gaa aat cat ttc aga tgacagtgtt taaccatggt	1694
Pro Cys Ala Cys Ala Lys Glu Asn His Phe Arg	
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aattcaaatt aaactgggtg tctttttctt ttcatctggc aaccctacta agatcataaa	1994
cccttggaaa tctgtgtgtg tgcgggtgtg tgtgtgtgtg tgtgtgcagg ggtggcagaa	2054
gtactgtggg atgggacaga aataagaaaa gatggaaaaa agaaaaagaac tctggaaatg	2114


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gatatccgaa aattttaaca gcaatttgta tagtattaaa taactttggc caggtgcggt 2294
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Pro Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu
      35              40              45

Gln Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn
50              55              60

Gly Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala
65              70              75              80

Pro Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr
      85              90              95

Thr Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu
100              105              110

Asn Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg
115              120              125

Gly Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser
130              135              140

Pro Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro
145              150              155              160

Asp Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp
165              170              175

Ala His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val
180              185              190

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	210					215					220				
Asp	Glu	Ile	Arg	Lys	Arg	Val	Phe	Glu	Met	Ala	Asn	Tyr	Val	Asn	Met
225					230					235					240
Leu	Tyr	Lys	Lys	Leu	Asn	Thr	His	Val	Ala	Leu	Val	Gly	Met	Glu	Ile
				245					250					255	
Trp	Thr	Asp	Lys	Asp	Lys	Ile	Lys	Ile	Thr	Pro	Asn	Ala	Ser	Phe	Thr
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Leu	Glu	Asn	Phe	Ser	Lys	Trp	Arg	Gly	Ser	Val	Leu	Ser	Arg	Arg	Lys
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Arg	His	Asp	Ile	Ala	Gln	Leu	Ile	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Thr
	290					295					300				
Thr	Val	Gly	Leu	Ala	Phe	Met	Ser	Thr	Met	Cys	Ser	Pro	Tyr	Ser	Val
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Gly	Val	Val	Gln	Asp	His	Ser	Asp	Asn	Leu	Leu	Arg	Val	Ala	Gly	Thr
			325						330					335	
Met	Ala	His	Glu	Met	Gly	His	Asn	Phe	Gly	Met	Phe	His	Asp	Asp	Tyr
			340					345					350		
Ser	Cys	Lys	Cys	Pro	Ser	Thr	Ile	Cys	Val	Met	Asp	Lys	Ala	Leu	Ser
		355					360					365			
Phe	Tyr	Ile	Pro	Thr	Asp	Phe	Ser	Ser	Cys	Ser	Arg	Leu	Ser	Tyr	Asp
	370					375					380				
Lys	Phe	Phe	Glu	Asp	Lys	Leu	Ser	Asn	Cys	Leu	Phe	Asn	Ala	Pro	Leu
385					390					395					400
Pro	Thr	Asp	Ile	Ile	Ser	Thr	Pro	Ile	Cys	Gly	Asn	Gln	Leu	Val	Glu
			405						410					415	
Met	Gly	Glu	Asp	Cys	Asp	Cys	Gly	Thr	Ser	Glu	Glu	Cys	Thr	Asn	Ile
			420					425					430		
Cys	Cys	Asp	Ala	Lys	Thr	Cys	Lys	Ile	Lys	Ala	Thr	Phe	Gln	Cys	Ala
		435					440					445			
Leu	Gly	Glu	Cys	Cys	Glu	Lys	Cys	Gln	Phe	Lys	Lys	Ala	Gly	Met	Val
	450					455					460				
Cys	Arg	Pro	Ala	Lys	Asp	Glu	Cys	Asp	Leu	Pro	Glu	Met	Cys	Asn	Gly
465					470					475					480
Lys	Ser	Gly	Asn	Cys	Pro	Asp	Asp	Arg	Phe	Gln	Val	Asn	Gly	Phe	Pro
			485						490				495		
Cys	His	His	Gly	Lys	Gly	His	Cys	Leu	Met	Gly	Thr	Cys	Pro	Thr	Leu
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of SEQ ID NO:1

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Leu Gln Gly Leu Leu Pro Val Ser Leu Leu Leu Ser Val Ala Val Ser
5 10 15

gct ata aaa gaa ctc cct ggg gtg aag aag tat gaa gtg gtt tat cct 153
Ala Ile Lys Glu Leu Pro Gly Val Lys Lys Tyr Glu Val Val Tyr Pro
20 25 30

ata aga ctt cat cca ctg cat aaa aga gag gcc aaa gag cca gag caa 201
Ile Arg Leu His Pro Leu His Lys Arg Glu Ala Lys Glu Pro Glu Gln
35 40 45

cag gaa caa ttt gaa act gaa tta aag tat aaa atg aca att aat gga 249
Gln Glu Gln Phe Glu Thr Glu Leu Lys Tyr Lys Met Thr Ile Asn Gly
50 55 60 65

aaa att gca gtg ctt tat ttg aaa aaa aac aag aac ctc ctt gca cca 297
Lys Ile Ala Val Leu Tyr Leu Lys Lys Asn Lys Asn Leu Leu Ala Pro
70 75 80

ggc tac acg gaa aca tat tat aat tcc act gga aag gag atc acc aca 345
Gly Tyr Thr Glu Thr Tyr Tyr Asn Ser Thr Gly Lys Glu Ile Thr Thr
85 90 95

agc cca caa att atg gat gat tgt tat tat caa gga cat att ctt aat 393
Ser Pro Gln Ile Met Asp Asp Cys Tyr Tyr Gln Gly His Ile Leu Asn

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gaa aag gtt tct gac gct agc atc agc aca tgt agg ggt cta agg ggc Glu Lys Val Ser Asp Ala Ser Ile Ser Thr Cys Arg Gly Leu Arg Gly 115 120 125			441
tac ttc agt cag ggg gat caa aga tac ttt att gaa cct tta agc ccc Tyr Phe Ser Gln Gly Asp Gln Arg Tyr Phe Ile Glu Pro Leu Ser Pro 130 135 140 145			489
ata cat cgg gat gga cag gag cat gca ctc ttc aag tat aac cct gat Ile His Arg Asp Gly Gln Glu His Ala Leu Phe Lys Tyr Asn Pro Asp 150 155 160			537
gaa aag aat tat gac agc acc tgt ggg atg gat ggt gtg ttg tgg gcc Glu Lys Asn Tyr Asp Ser Thr Cys Gly Met Asp Gly Val Leu Trp Ala 165 170 175			585
cac gat ttg cag cag aac att gcc cta cct gcc acc aaa cta gta aaa His Asp Leu Gln Gln Asn Ile Ala Leu Pro Ala Thr Lys Leu Val Lys 180 185 190			633
ttg aaa gac agg aag gtt cag gaa cat gag aaa tac ata gaa tat tat Leu Lys Asp Arg Lys Val Gln Glu His Glu Lys Tyr Ile Glu Tyr Tyr 195 200 205			681
ttg gtc ctg gat aat ggt gag ttt aaa agg tac aat gag aat caa gat Leu Val Leu Asp Asn Gly Glu Phe Lys Arg Tyr Asn Glu Asn Gln Asp 210 215 220 225			729
gag atc aga aag agg gta ttt gag atg gct aat tat gtc aac atg ctt Glu Ile Arg Lys Arg Val Phe Glu Met Ala Asn Tyr Val Asn Met Leu 230 235 240			777
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Ser	Gln	Glu	Ile	Gly	Met	Val	Ala	Asn	Gly	Thr	Lys	Cys	Gly	Asp	Asn		
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Lys	Val	Cys	Ile	Asn	Ala	Glu	Cys	Val	Asp	Ile	Glu	Lys	Ala	Tyr	Lys		
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Pro	Val	Glu	Gly	Asn	Glu	Pro	Pro	Ala	Ser	Phe	His	Lys	Asp	Thr	Asn		
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Ala	Leu	Pro	Pro	Thr	Val	Phe	Lys	Asp	Asn	Pro	Met	Ser	Thr	Pro	Lys		
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Asp	Ser	Asn	Pro	Lys	Ala												
770					775												
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Pro	Ile	Arg	Leu	His	Pro	Leu	His	Lys	Arg	Glu	Ala	Lys	Glu	Pro	Glu	35	40	45	
Gln	Gln	Glu	Gln	Phe	Glu	Thr	Glu	Leu	Lys	Tyr	Lys	Met	Thr	Ile	Asn	50	55	60	
Gly	Lys	Ile	Ala	Val	Leu	Tyr	Leu	Lys	Lys	Asn	Lys	Asn	Leu	Leu	Ala	65	70	75	80
Pro	Gly	Tyr	Thr	Glu	Thr	Tyr	Tyr	Asn	Ser	Thr	Gly	Lys	Glu	Ile	Thr	85	90	95	
Thr	Ser	Pro	Gln	Ile	Met	Asp	Asp	Cys	Tyr	Tyr	Gln	Gly	His	Ile	Leu	100	105	110	
Asn	Glu	Lys	Val	Ser	Asp	Ala	Ser	Ile	Ser	Thr	Cys	Arg	Gly	Leu	Arg	115	120	125	
Gly	Tyr	Phe	Ser	Gln	Gly	Asp	Gln	Arg	Tyr	Phe	Ile	Glu	Pro	Leu	Ser	130	135	140	
Pro	Ile	His	Arg	Asp	Gly	Gln	Glu	His	Ala	Leu	Phe	Lys	Tyr	Asn	Pro	145	150	155	160
Asp	Glu	Lys	Asn	Tyr	Asp	Ser	Thr	Cys	Gly	Met	Asp	Gly	Val	Leu	Trp	165	170	175	
Ala	His	Asp	Leu	Gln	Gln	Asn	Ile	Ala	Leu	Pro	Ala	Thr	Lys	Leu	Val	180	185	190	
Lys	Leu	Lys	Asp	Arg	Lys	Val	Gln	Glu	His	Glu	Lys	Tyr	Ile	Glu	Tyr	195	200	205	
Tyr	Leu	Val	Leu	Asp	Asn	Gly	Glu	Phe	Lys	Arg	Tyr	Asn	Glu	Asn	Gln	210	215	220	
Asp	Glu	Ile	Arg	Lys	Arg	Val	Phe	Glu	Met	Ala	Asn	Tyr	Val	Asn	Met	225	230	235	240

Leu Tyr Lys Lys Leu Asn Thr His Val Ala Leu Val Gly Met Glu Ile
 245 250 255
 Trp Thr Asp Lys Asp Lys Ile Lys Ile Thr Pro Asn Ala Ser Phe Thr
 260 265 270
 Leu Glu Asn Phe Ser Lys Trp Arg Gly Ser Val Leu Ser Arg Arg Lys
 275 280 285
 Arg His Asp Ile Ala Gln Leu Ile Thr Ala Thr Glu Leu Ala Gly Thr
 290 295 300
 Thr Val Gly Leu Ala Phe Met Ser Thr Met Cys Ser Pro Tyr Ser Val
 305 310 315 320
 Gly Val Val Gln Asp His Ser Asp Asn Leu Leu Arg Val Ala Gly Thr
 325 330 335
 Met Ala His Glu Met Gly His Asn Phe Gly Met Phe His Asp Asp Tyr
 340 345 350
 Ser Cys Lys Cys Pro Ser Thr Ile Cys Val Met Asp Lys Ala Leu Ser
 355 360 365
 Phe Tyr Ile Pro Thr Asp Phe Ser Ser Cys Ser Arg Leu Ser Tyr Asp
 370 375 380
 Lys Phe Phe Glu Asp Lys Leu Ser Asn Cys Leu Phe Asn Ala Pro Leu
 385 390 395 400
 Pro Thr Asp Ile Ile Ser Thr Pro Ile Cys Gly Asn Gln Leu Val Glu
 405 410 415
 Met Gly Glu Asp Cys Asp Cys Gly Thr Ser Glu Glu Cys Thr Asn Ile
 420 425 430
 Cys Cys Asp Ala Lys Thr Cys Lys Ile Lys Ala Thr Phe Gln Cys Ala
 435 440 445
 Leu Gly Glu Cys Cys Glu Lys Cys Gln Phe Lys Lys Ala Gly Met Val
 450 455 460
 Cys Arg Pro Ala Lys Asp Glu Cys Asp Leu Pro Glu Met Cys Asn Gly
 465 470 475 480
 Lys Ser Gly Asn Cys Pro Asp Asp Arg Phe Gln Val Asn Gly Phe Pro
 485 490 495
 Cys His His Gly Lys Gly His Cys Leu Met Gly Thr Cys Pro Thr Leu
 500 505 510
 Gln Glu Gln Cys Thr Glu Leu Trp Gly Pro Gly Thr Glu Val Ala Asp
 515 520 525
 Lys Ser Cys Tyr Asn Arg Asn Glu Gly Gly Ser Lys Tyr Gly Tyr Cys
 530 535 540
 Arg Arg Val Asp Asp Thr Leu Ile Pro Cys Lys Ala Asn Asp Thr Met
 545 550 555 560

Cys	Gly	Lys	Leu	Phe	Cys	Gln	Gly	Gly	Ser	Asp	Asn	Leu	Pro	Trp	Lys	
				565					570					575		
Gly	Arg	Ile	Val	Thr	Phe	Leu	Thr	Cys	Lys	Thr	Phe	Asp	Pro	Glu	Asp	
			580					585					590			
Thr	Ser	Gln	Glu	Ile	Gly	Met	Val	Ala	Asn	Gly	Thr	Lys	Cys	Gly	Asp	
		595					600					605				
Asn	Lys	Val	Cys	Ile	Asn	Ala	Glu	Cys	Val	Asp	Ile	Glu	Lys	Ala	Tyr	
	610					615					620					
Lys	Ser	Thr	Asn	Cys	Ser	Ser	Lys	Cys	Lys	Gly	His	Ala	Val	Cys	Asp	
625					630					635					640	
His	Glu	Leu	Gln	Cys	Gln	Cys	Glu	Glu	Gly	Trp	Ile	Pro	Pro	Asp	Cys	
			645						650					655		
Asp	Asp	Ser	Ser	Val	Val	Phe	His	Phe	Ser	Ile	Val	Val	Gly	Val	Leu	
			660					665					670			
Phe	Pro	Met	Ala	Val	Ile	Phe	Val	Val	Val	Ala	Met	Val	Ile	Arg	His	
		675					680					685				
Gln	Ser	Ser	Arg	Glu	Lys	Gln	Lys	Lys	Asp	Gln	Arg	Pro	Leu	Ser	Thr	
	690					695					700					
Thr	Gly	Thr	Arg	Pro	His	Lys	Gln	Lys	Arg	Lys	Pro	Gln	Met	Val	Lys	
705					710					715					720	
Ala	Val	Gln	Pro	Gln	Glu	Met	Ser	Gln	Met	Lys	Pro	His	Val	Tyr	Asp	
				725					730					735		
Leu	Pro	Val	Glu	Gly	Asn	Glu	Pro	Pro	Ala	Ser	Phe	His	Lys	Asp	Thr	
		740						745					750			
Asn	Ala	Leu	Pro	Pro	Thr	Val	Phe	Lys	Asp	Asn	Pro	Met	Ser	Thr	Pro	
	755						760					765				
Lys	Asp	Ser	Asn	Pro	Lys	Ala										
	770					775										